INPUT SET: S32774.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)     General Information:                      ENTERED
 4
 5      (i) APPLICANT: Jiang, Min
 6                     Potter, Andrew A.
 7                     MacLachlan, Philip R.
 8
 9     (ii) TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
10
11    (iii) NUMBER OF SEQUENCES: 4
12
13     (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: Reed & Robins LLP
15           (B) STREET: 285 Hamilton Avenue, Suite 200
16           (C) CITY: Palo Alto
17           (D) STATE: California
18           (E) COUNTRY: USA
19           (F) ZIP: 94301
20
21      (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Floppy disk
23           (B) COMPUTER: IBM PC compatible
24           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27     (vi) CURRENT APPLICATION DATA:
28           (A) APPLICATION NUMBER: 09/234,733
29           (B) FILING DATE:
30           (C) CLASSIFICATION:
31
32    (vii) PRIOR APPLICATION DATA:
33           (A) APPLICATION NUMBER:  08/658,277
34           (B) FILING DATE:
35
36   (viii) ATTORNEY/AGENT INFORMATION:
37           (A) NAME: Robins, Roberta L.
38           (B) REGISTRATION NUMBER: 33,208
39           (C) REFERENCE/DOCKET NUMBER: 9000-0030
40
41     (ix) TELECOMMUNICATION INFORMATION:
42           (A) TELEPHONE: (415) 327-3400
43           (B) TELEFAX: (415) 327 3231
44
```

```
47
48        (i) SEQUENCE CHARACTERISTICS:
49            (A) LENGTH: 1191 base pairs
50            (B) TYPE: nucleic acid
51            (C) STRANDEDNESS: single
52            (D) TOPOLOGY: linear
53
54      (ii) MOLECULE TYPE: DNA (genomic)
55
56
57      (ix) FEATURE:
58            (A) NAME/KEY: CDS
59            (B) LOCATION: 157..924
60
61
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64  AATGAACATA AAATAAAAAT TAATAATTAT ATATTTTTAT GATAATCACA TATATTTGAC        60
65
66  TTAAAAAAAT TGTTACTGTA TGATACAGGC ATAAGTACTT ATTTATTTTA TAGATTGCAA       120
67
68  TTTATAAACA ATTATATTTT TCAAAGAGGA ATGCTT ATG GAA TTC AAA AAG TTA        174
69                                         Met Glu Phe Lys Lys Leu
70                                          1               5
71
72  CTT TAT TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT        222
73  Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile
74              10                  15                  20
75
76  TTA ACA AGT GTC CAA GCA AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT        270
77  Leu Thr Ser Val Gln Ala Asn Gln Ile Asn Val Ser Gln Pro Ser Asn
78          25                  30                  35
79
80  AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA GAA GAA ATT GAT AAT AGT        318
81  Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser
82          40                  45                  50
83
84  CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT GTT AAA        366
85  Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys
86      55                  60                  65                  70
87
88  GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA        414
89  Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu
90                  75                  80                  85
91
92  AAT TTA AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA        462
93  Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu
94              90                  95                  100
95
96  AAT TCG ATT GGA ACA AGA GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA        510
97  Asn Ser Ile Gly Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala
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101   Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His
102       120             125             130
103
104   ATT GAT ATG GGA TTT GCT ATT ACG AAA TTA CTT ATT CGC ATT GCA GAC        606
105   Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp
106   135             140             145             150
107
108   CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA        654
109   Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys
110                   155             160             165
111
112   CAA GTG CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT        702
113   Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp
114               170             175             180
115
116   AGA GCA ACT ATT TAC GTT AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA        750
117   Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln
118           185             190             195
119
120   ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT AAT GTA AAG AGT TTT GAA        798
121   Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu
122       200             205             210
123
124   GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT GTA CAA        846
125   Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln
126   215             220             225             230
127
128   TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG        894
129   Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val
130               235             240             245
131
132   CTA CAA GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAG ATTGAATTGA          944
133   Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
134               250             255
135
136   CGTATTAAAA AGGACTGGAA TTTATTAATT TCAGTCCTTT AGAATTTTTA TTTAGCTGAT     1004
137
138   TTACTTGTTG AAGAGATTTG GTGGAAAATC AAGTACCATA CTTCATTTCT CCTCCAAATA     1064
139
140   CTTGTATGTC GATTCCCTTC TAAAACATAG CTAATTAGTT TAGTTTTCTG CCTAATAGAT     1124
141
142   TGTACATGAA ATTGTTCAAA ATTACTAGGG TAAAAGGTTT TTCTTTTTAT AAATTCATCA     1184
143
144   TGACTAT                                                              1191
145
146
147   (2) INFORMATION FOR SEQ ID NO:2:
148
149       (i) SEQUENCE CHARACTERISTICS:
150           (A) LENGTH: 256 amino acids
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153
154        (ii) MOLECULE TYPE: protein
155
156        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
157
158   Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
159    1           5                  10                  15
160
161   Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
162              20                  25                  30
163
164   Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
165              35                  40                  45
166
167   Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
168          50                  55                  60
169
170   Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
171    65                  70                  75                  80
172
173   Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
174              85                  90                  95
175
176   Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
177              100                 105                 110
178
179   Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
180              115                 120                 125
181
182   Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
183              130                 135                 140
184
185   Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
186    145                 150                 155                 160
187
188   Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
189              165                 170                 175
190
191   Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
192              180                 185                 190
193
194   Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
195              195                 200                 205
196
197   Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
198              210                 215                 220
199
200   His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
201    225                 230                 235                 240
202
20_   A__ ___ ___ ___ ___ Val ___ ___ ___ Ala Leu Asn Thr Ala Leu Gln
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PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/234,733*

DATE: 08/04/1999
TIME: 14:39:34

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206
207   (2) INFORMATION FOR SEQ ID NO:3:
208
209       (i)  SEQUENCE CHARACTERISTICS:
210            (A)  LENGTH: 256 amino acids
211            (B)  TYPE: amino acid
212            (C)  STRANDEDNESS: single
213            (D)  TOPOLOGY: linear
214
215      (ii) MOLECULE TYPE: protein
216
217
218
219
220      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
221
222   Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
223   1               5                   10                  15
224
225   Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
226               20                  25                  30
227
228   Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
229           35                  40                  45
230
231   Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
232       50                  55                  60
233
234   Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
235   65                  70                  75                  80
236
237   Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
238               85                  90                  95
239
240   Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
241               100                 105                 110
242
243   Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
244           115                 120                 125
245
246   Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
247           130                 135                 140
248
249   Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
250   145                 150                 155                 160
251
252   Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
253           165                 170                 175
254
255   Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
256           180                 185                 190
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/234,733*

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Line   Error   Original Text

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/09/234,733*

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/09/234,733*

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Line   Original Text   Corrected Text